



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 02:00 AM UTC

PDB ID : 1NTC / pdb_00001ntc
Title : SOLUTION STRUCTURE OF THE DNA-BINDING DOMAIN OF NTRC
WITH THREE ALANINE SUBSTITUTIONS
Authors : Pelton, J.G.; Kustu, S.; Wemmer, D.E.
Deposited on : 1999-05-26

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

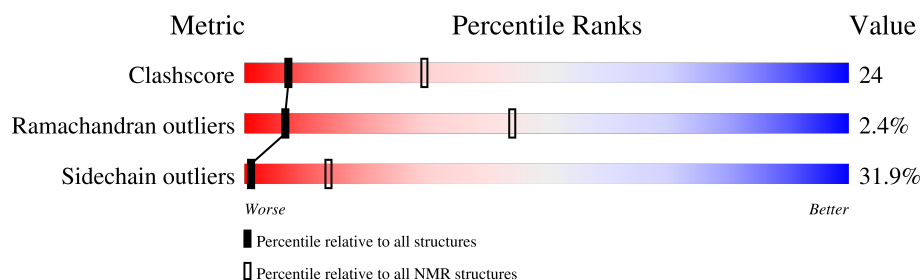
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	91	35% 34% • 27%
1	B	91	35% 34% • 27%

2 Ensemble composition and analysis

This entry contains 28 models. Model 3 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:402-A:467, B:402-B:467 (132)	0.65	3

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 5, 6, 8, 9, 11, 12, 13, 15, 16, 17, 19, 20, 21, 22, 26, 27
2	2, 4, 14, 18, 24
3	7, 10, 23
Single-model clusters	25; 28

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2794 atoms, of which 1388 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (NITROGEN REGULATION PROTEIN (NTRC)).

Mol	Chain	Residues	Atoms						Trace
1	A	91	Total	C	H	N	O	S	0
			1397	439	694	126	136	2	
1	B	91	Total	C	H	N	O	S	0
			1397	439	694	126	136	2	

There are 8 discrepancies between the modelled and reference sequences:

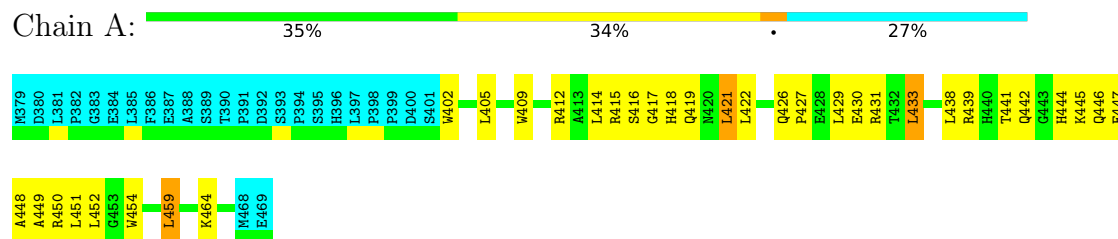
Chain	Residue	Modelled	Actual	Comment	Reference
A	379	MET	GLN	cloning artifact	UNP P41789
B	379	MET	GLN	cloning artifact	UNP P41789
A	456	ALA	ARG	engineered mutation	UNP P41789
B	456	ALA	ARG	engineered mutation	UNP P41789
A	457	ALA	ASN	engineered mutation	UNP P41789
B	457	ALA	ASN	engineered mutation	UNP P41789
A	461	ALA	ARG	engineered mutation	UNP P41789
B	461	ALA	ARG	engineered mutation	UNP P41789

4 Residue-property plots

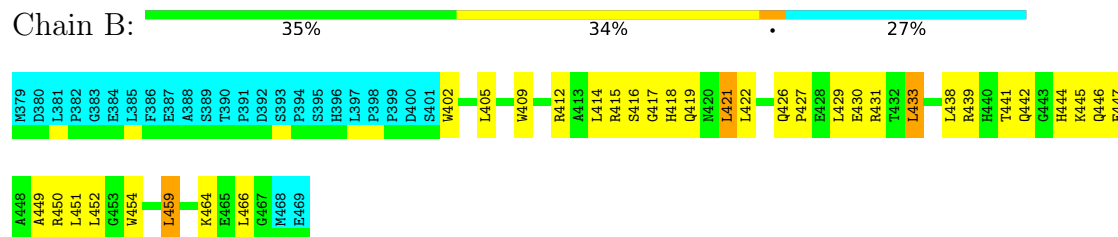
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

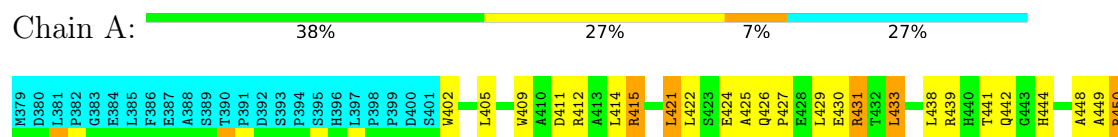


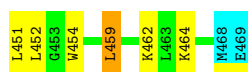
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))





- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

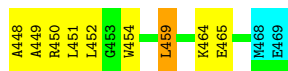
Chain B: 37% 29% 7% 27%



4.2.2 Score per residue for model 2

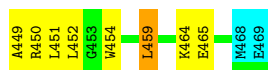
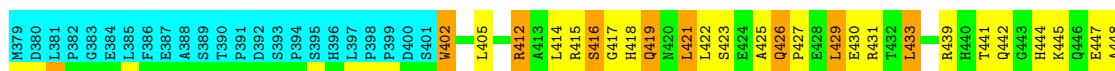
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 34% 29% 10% 27%



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain B: 35% 27% 10% 27%



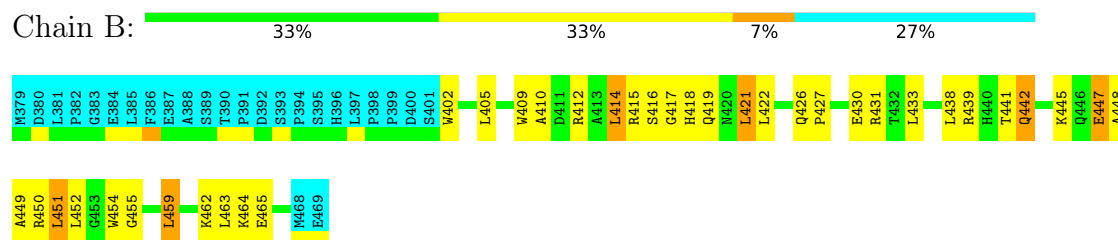
4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 33% 33% 7% 27%

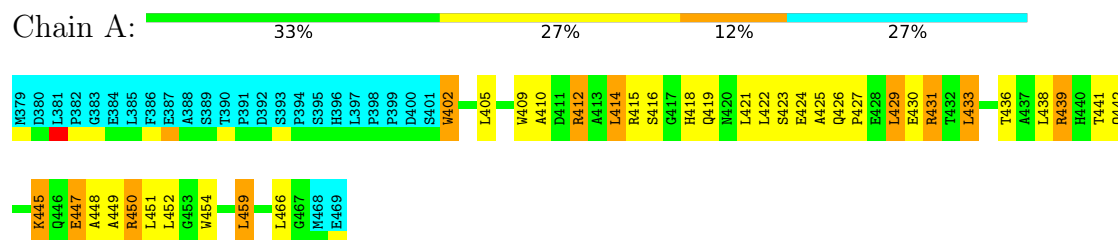


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

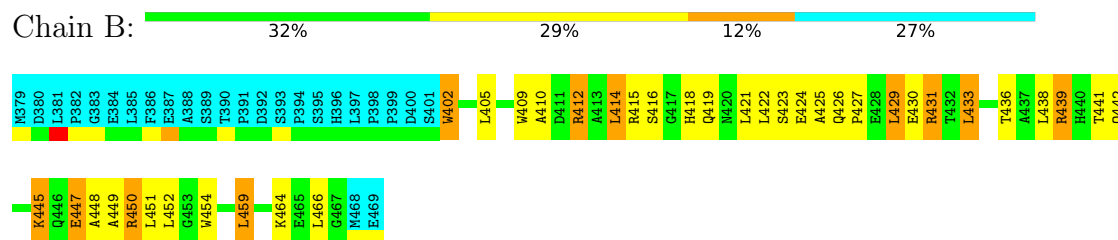


4.2.4 Score per residue for model 4

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

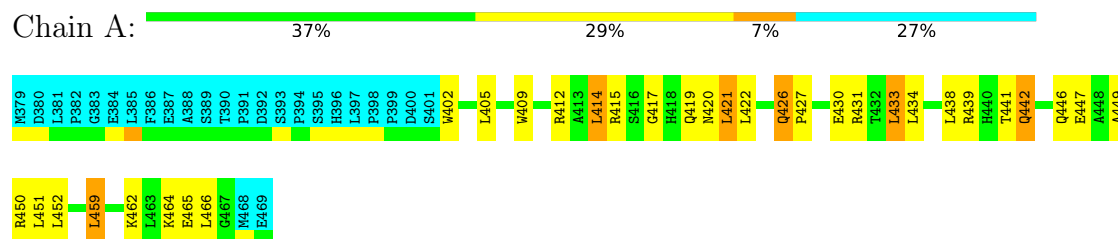


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

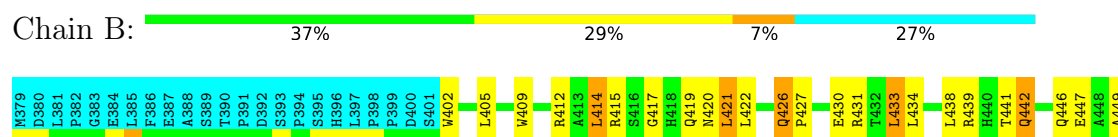


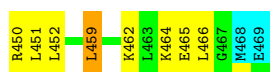
4.2.5 Score per residue for model 5

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



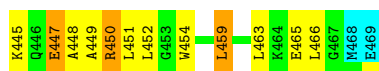
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



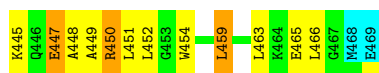
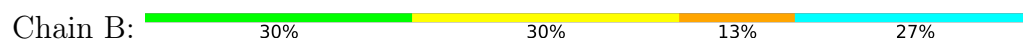


4.2.6 Score per residue for model 6

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

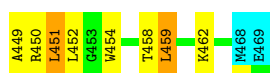


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

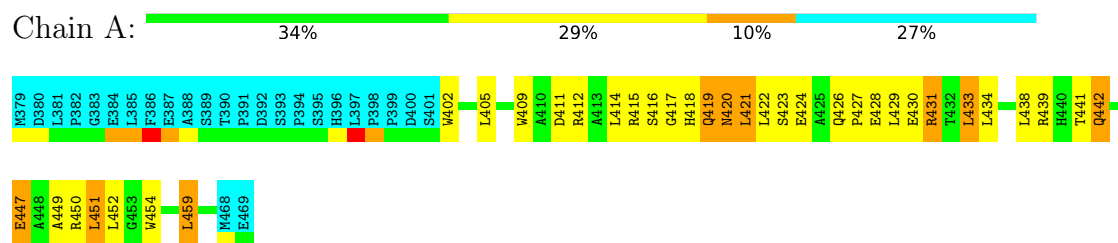


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

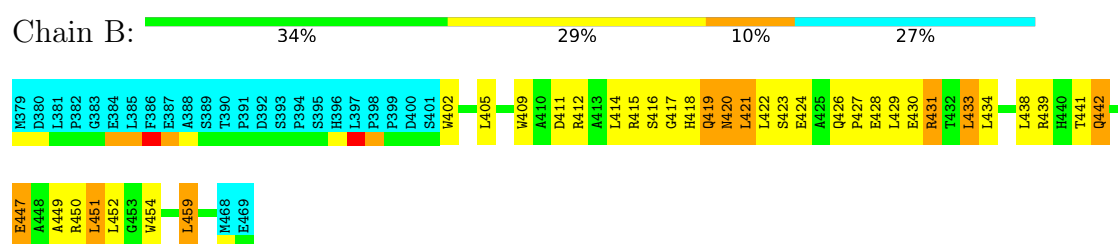


4.2.8 Score per residue for model 8

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

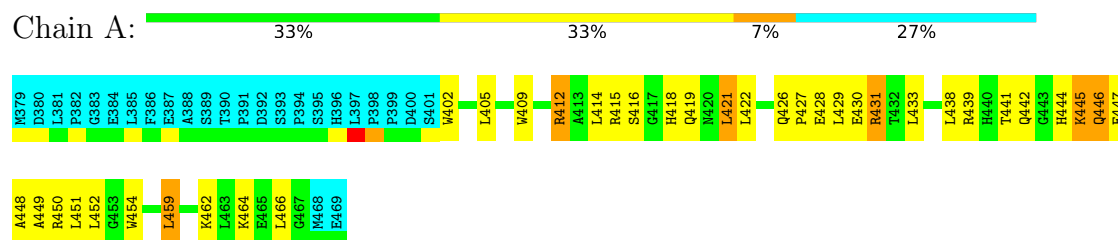


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

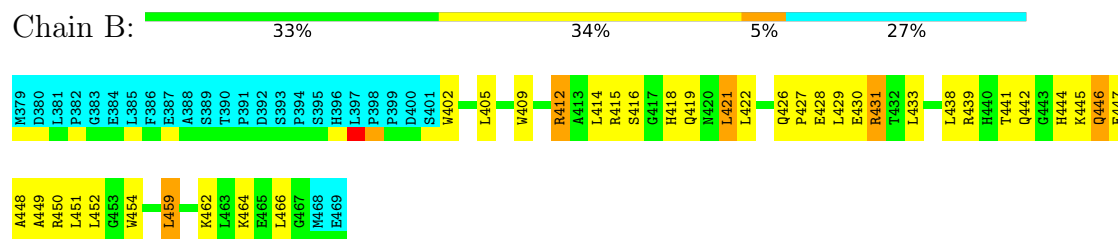


4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

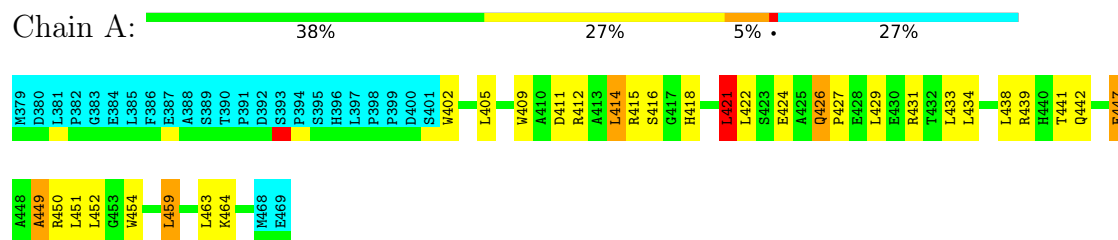


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

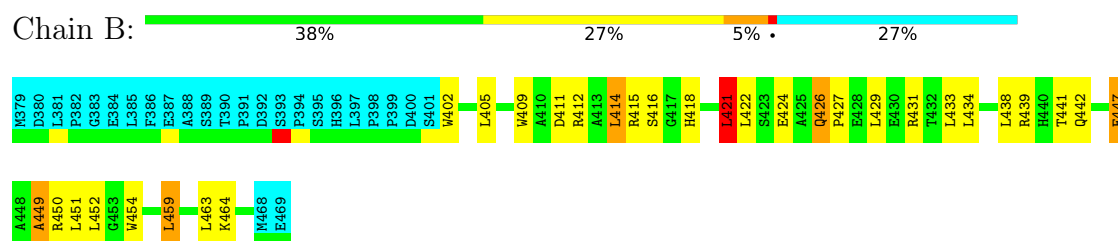


4.2.10 Score per residue for model 10

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

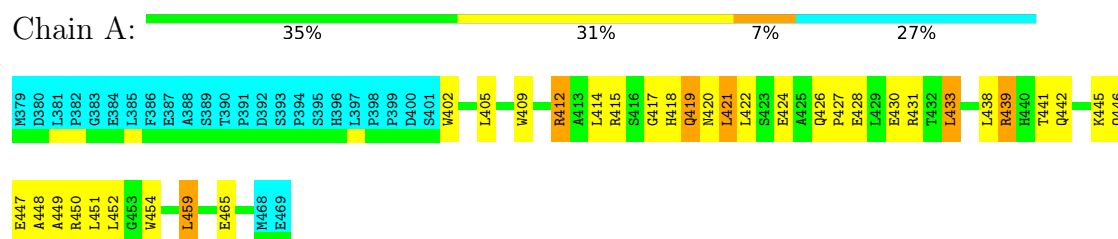


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

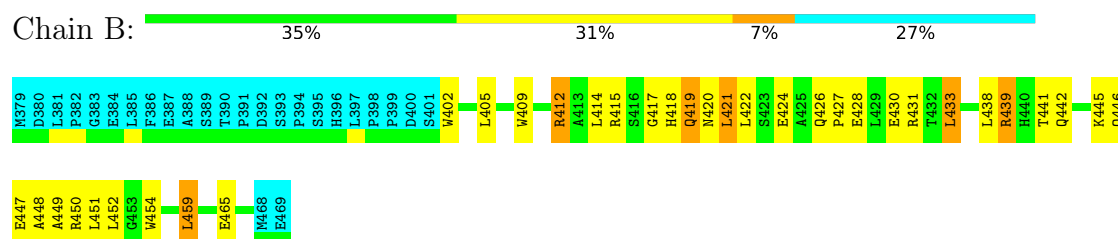


4.2.11 Score per residue for model 11

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

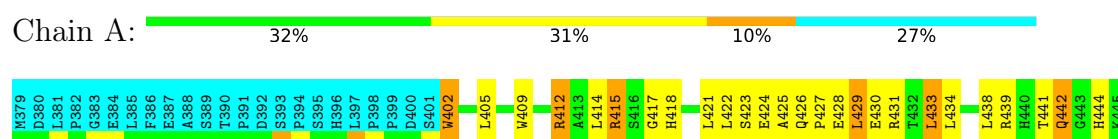


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



4.2.12 Score per residue for model 12

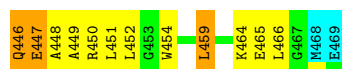
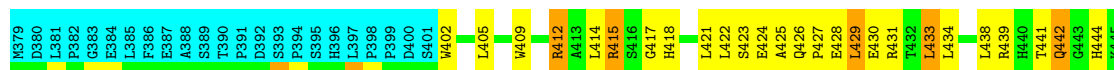
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))





- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

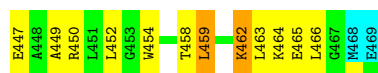
Chain B: 31% 33% 9% 27%



4.2.13 Score per residue for model 13

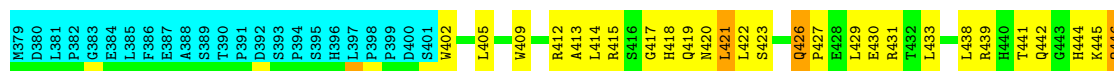
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 30% 36% 7% 27%



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain B: 30% 37% 5% 27%



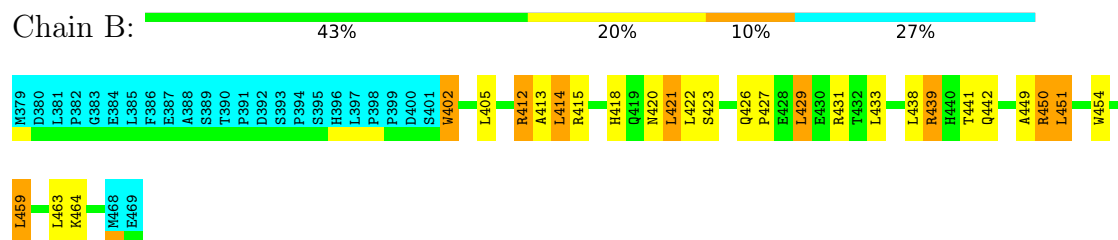
4.2.14 Score per residue for model 14

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 46% 16% 10% 27%

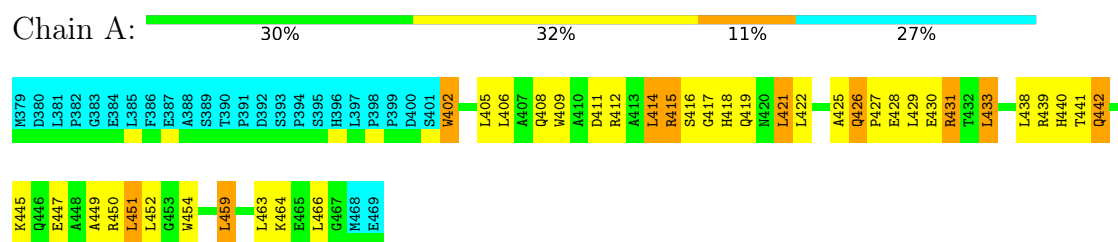


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

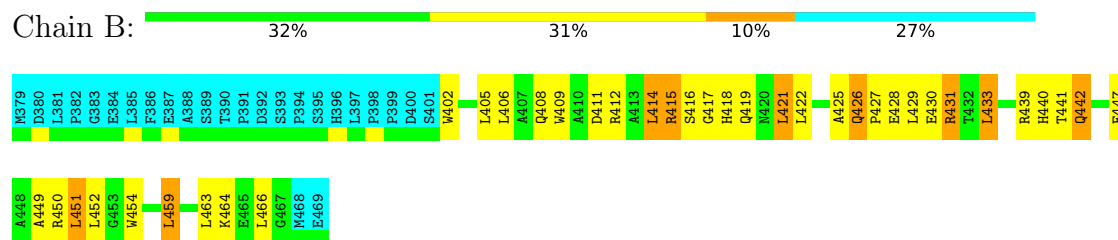


4.2.15 Score per residue for model 15

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

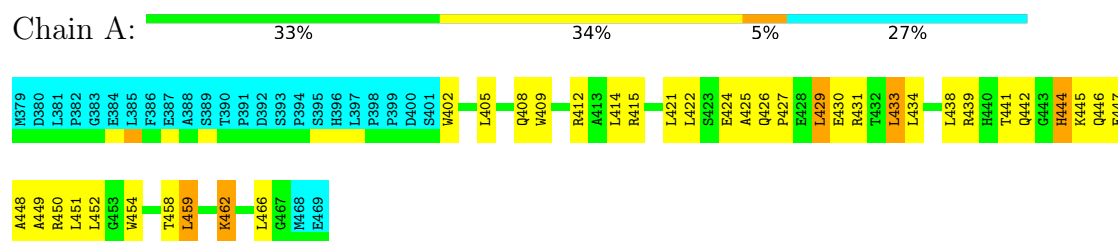


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

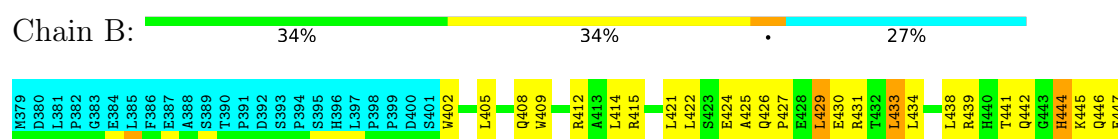


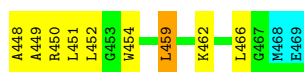
4.2.16 Score per residue for model 16

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

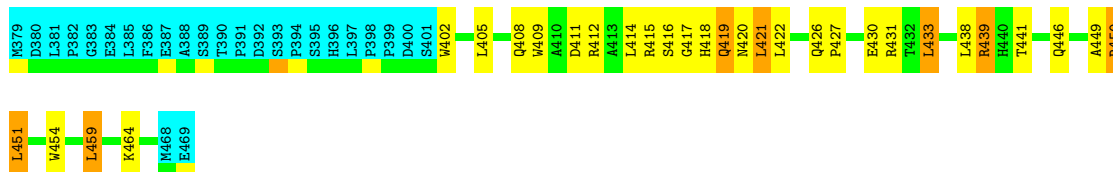




4.2.17 Score per residue for model 17

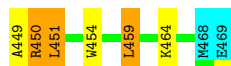
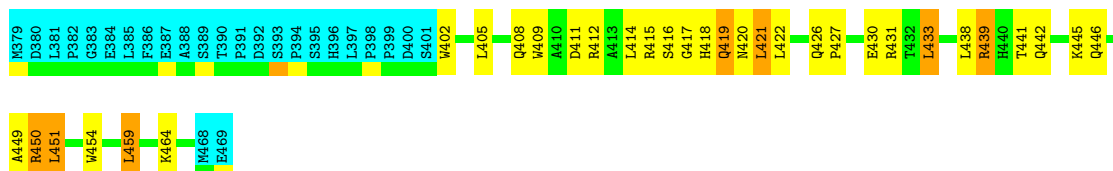
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 40% 25% 8% 27%



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

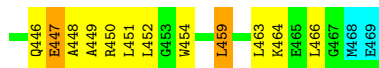
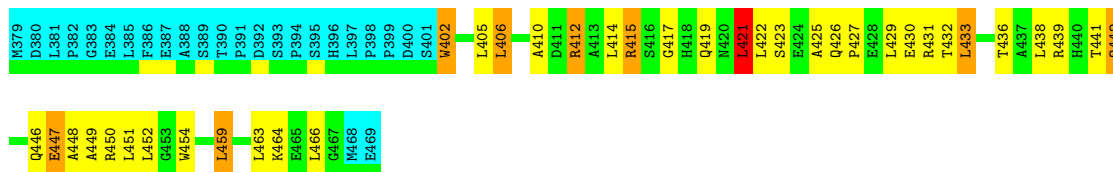
Chain B: 37% 27% 8% 27%



4.2.18 Score per residue for model 18

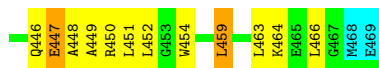
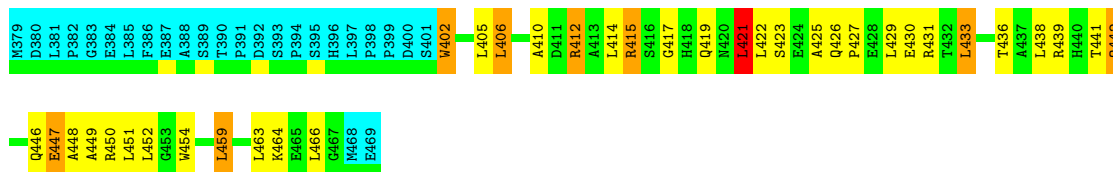
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 32% 31% 9% 27%



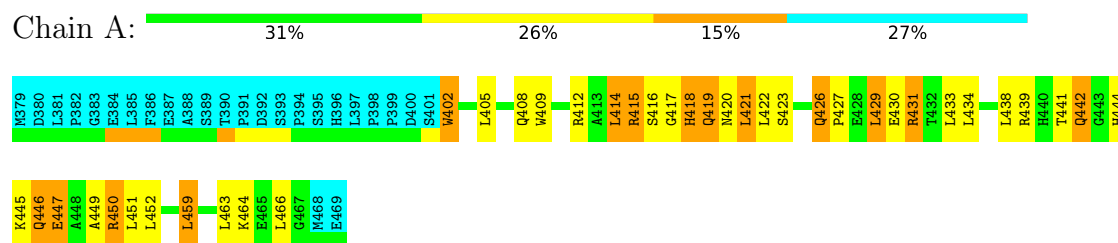
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain B: 33% 30% 9% 27%

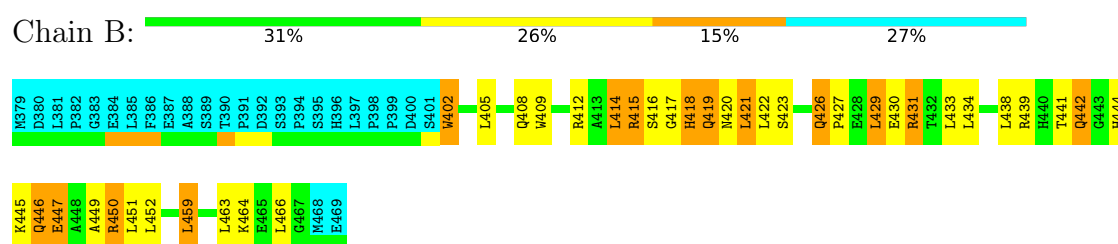


4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

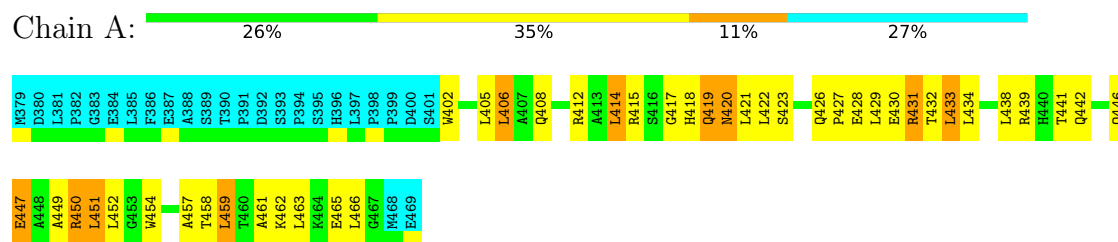


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

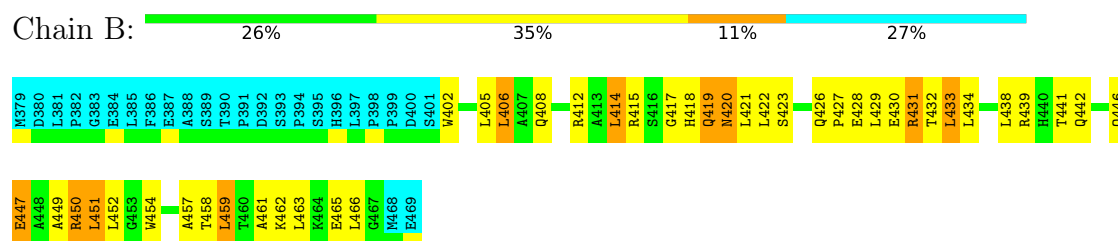


4.2.20 Score per residue for model 20

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

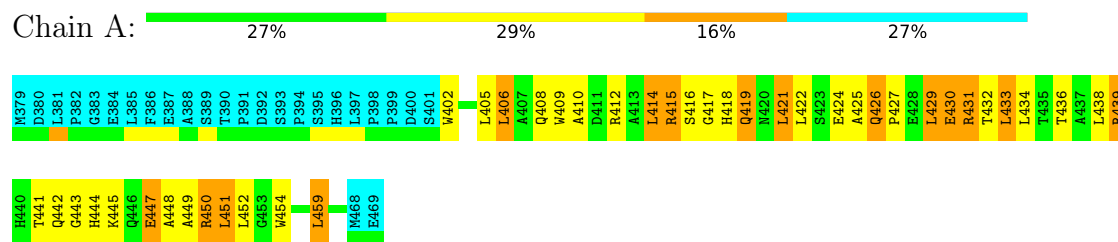


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

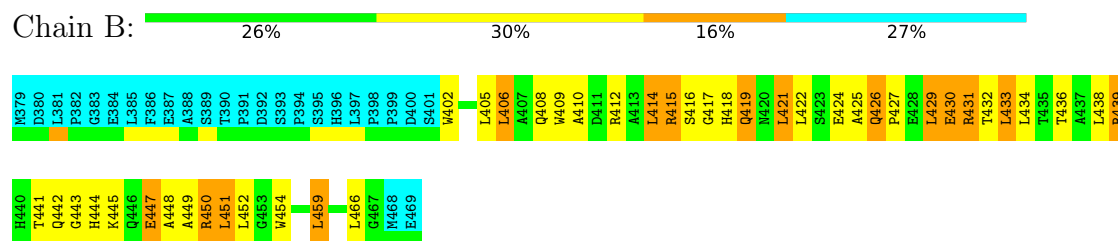


4.2.21 Score per residue for model 21

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

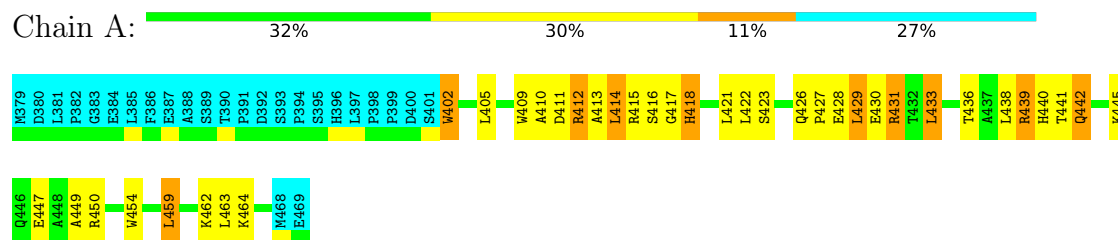


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

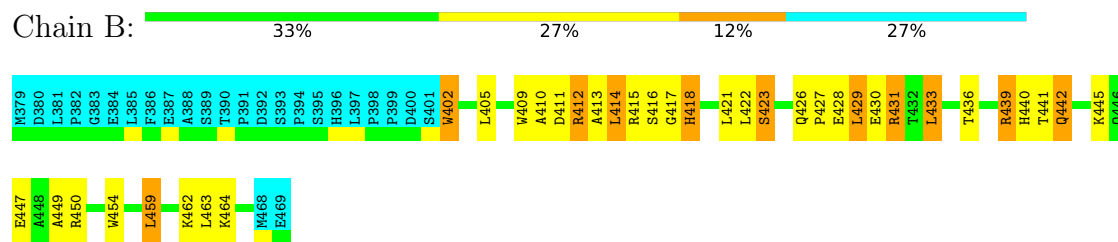


4.2.22 Score per residue for model 22

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

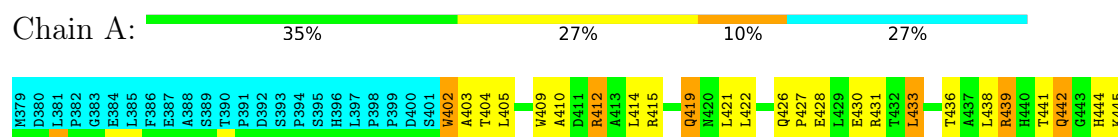


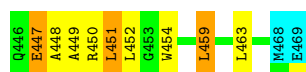
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



4.2.23 Score per residue for model 23

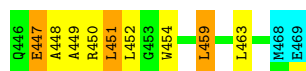
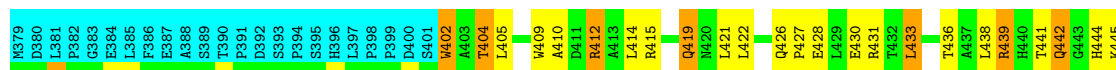
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))





- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

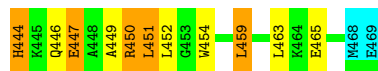
Chain B: 36% 25% 11% 27%



4.2.24 Score per residue for model 24

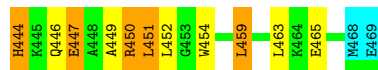
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 31% 30% 12% 27%



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

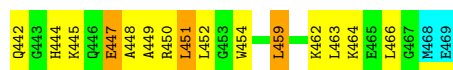
Chain B: 31% 30% 12% 27%



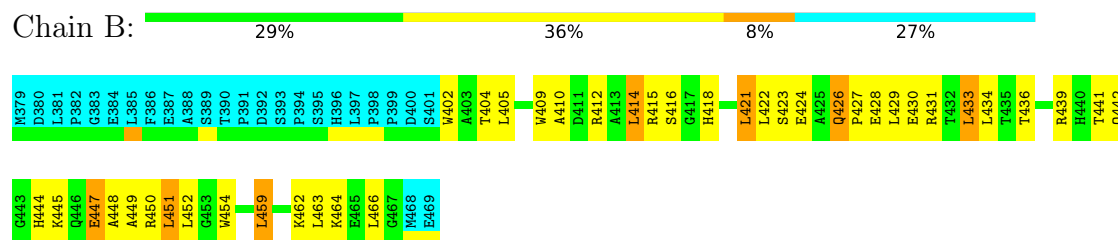
4.2.25 Score per residue for model 25

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 27% 37% 8% 27%

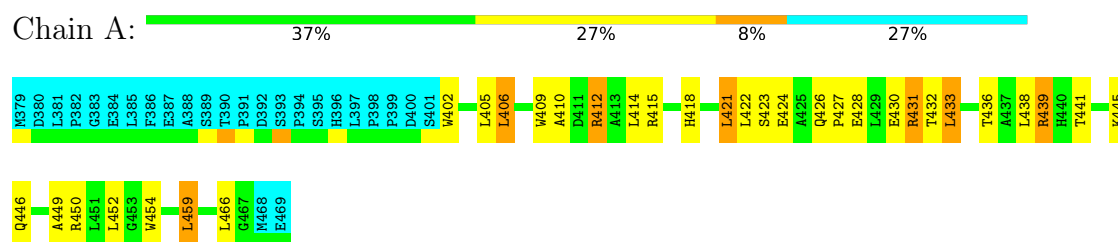


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

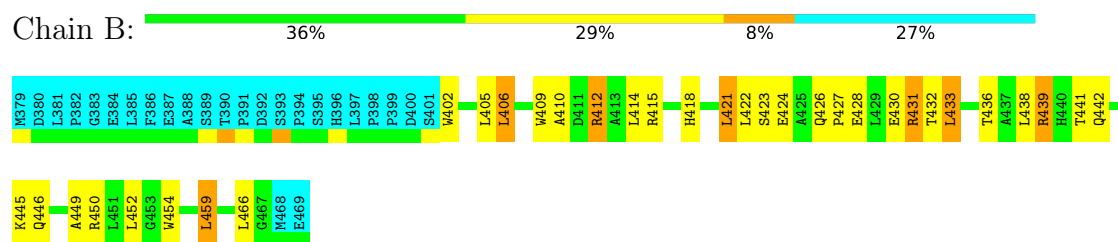


4.2.26 Score per residue for model 26

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

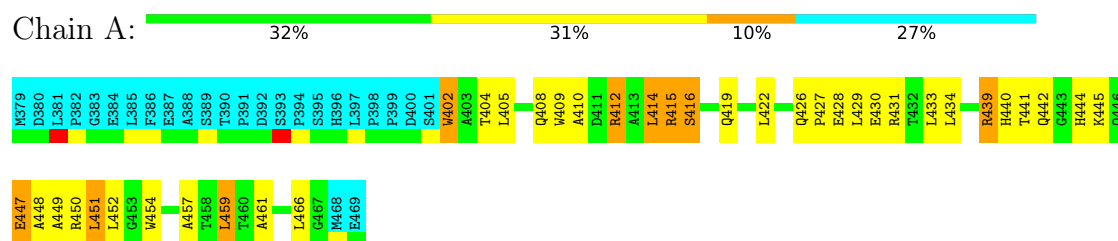


- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

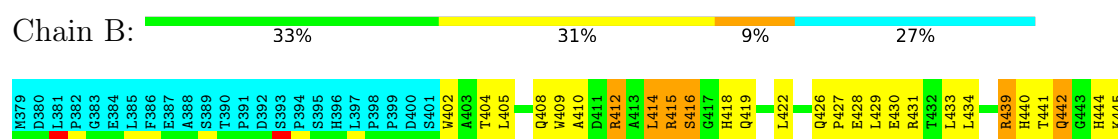


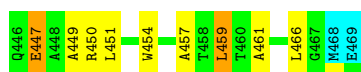
4.2.27 Score per residue for model 27

- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

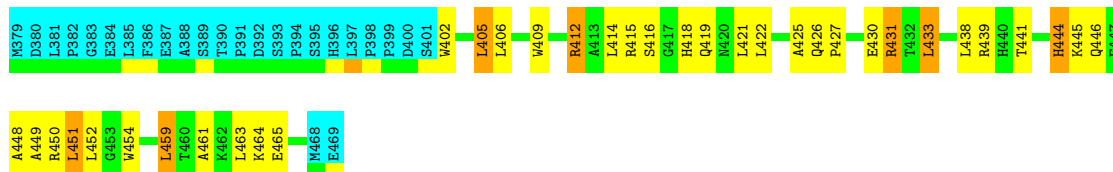




4.2.28 Score per residue for model 28

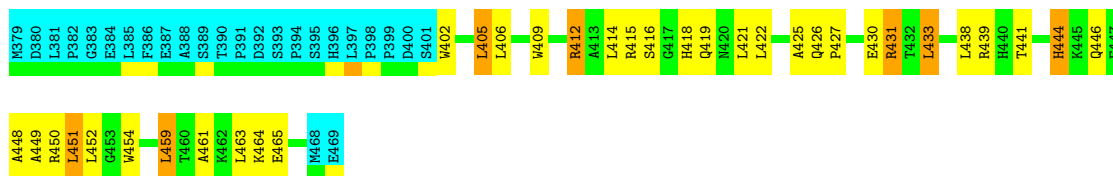
- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain A: 34% 31% 8% 27%



- Molecule 1: PROTEIN (NITROGEN REGULATION PROTEIN (NTRC))

Chain B: 35% 30% 8% 27%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 40 calculated structures, 28 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION AND LOW ENERGY*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	3.851
X-PLOR	structure solution	3.851

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.50±0.01	0±0/525 (0.0± 0.0%)	1.52±0.01	0±0/713 (0.0± 0.0%)
1	B	1.50±0.01	0±0/525 (0.0± 0.0%)	1.52±0.01	0±0/713 (0.0± 0.0%)
All	All	1.50	0/29400 (0.0%)	1.52	2/39928 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	5.0±0.0
1	B	0.0±0.0	5.0±0.0
All	All	0	280

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	416	SER	N-CA-CB	-5.73	104.91	111.79	6	1
1	A	416	SER	N-CA-CB	-5.65	105.01	111.79	6	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	412	ARG	Sidechain	28
1	A	415	ARG	Sidechain	28
1	A	431	ARG	Sidechain	28
1	A	439	ARG	Sidechain	28

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	450	ARG	Sidechain	28
1	B	412	ARG	Sidechain	28
1	B	415	ARG	Sidechain	28
1	B	431	ARG	Sidechain	28
1	B	439	ARG	Sidechain	28
1	B	450	ARG	Sidechain	28

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	515	525	525	31±6
1	B	515	525	525	31±6
All	All	28840	29400	29400	1370

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:422:LEU:HD13	1:B:454:TRP:CZ2	0.94	1.97	27	26
1:A:454:TRP:CZ2	1:B:422:LEU:HD13	0.94	1.97	27	26
1:A:433:LEU:HD12	1:A:452:LEU:CD2	0.86	2.00	20	15
1:B:433:LEU:HD12	1:B:452:LEU:CD2	0.85	2.01	20	15
1:A:405:LEU:HD13	1:A:405:LEU:O	0.84	1.73	20	27
1:B:405:LEU:HD13	1:B:405:LEU:O	0.84	1.72	20	27
1:A:425:ALA:HB1	1:B:429:LEU:HD11	0.82	1.52	18	10
1:A:410:ALA:O	1:A:414:LEU:HD12	0.81	1.76	3	1
1:A:429:LEU:HD11	1:B:425:ALA:HB1	0.81	1.52	18	10
1:B:410:ALA:O	1:B:414:LEU:HD12	0.81	1.76	3	1
1:B:449:ALA:HA	1:B:459:LEU:HD12	0.72	1.62	26	28
1:A:414:LEU:HD22	1:A:414:LEU:O	0.72	1.83	27	1
1:A:449:ALA:HA	1:A:459:LEU:HD12	0.72	1.62	26	28
1:B:414:LEU:HD22	1:B:414:LEU:O	0.72	1.84	27	1
1:B:449:ALA:CA	1:B:459:LEU:HD12	0.71	2.15	26	28
1:A:429:LEU:HD12	1:B:402:TRP:CZ3	0.71	2.21	2	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:418:HIS:CD2	1:B:451:LEU:HD23	0.71	2.21	17	2
1:A:449:ALA:CA	1:A:459:LEU:HD12	0.70	2.16	26	28
1:A:402:TRP:CZ3	1:B:429:LEU:HD12	0.70	2.21	2	7
1:A:433:LEU:HD23	1:B:406:LEU:HD21	0.70	1.62	28	2
1:A:452:LEU:HD22	1:B:422:LEU:CD1	0.69	2.16	6	11
1:A:454:TRP:CH2	1:B:422:LEU:HD13	0.69	2.22	10	18
1:A:406:LEU:HD21	1:B:433:LEU:HD23	0.69	1.62	28	2
1:A:433:LEU:HD23	1:B:406:LEU:CD1	0.69	2.18	21	3
1:A:422:LEU:CD1	1:B:452:LEU:HD22	0.69	2.17	6	11
1:A:422:LEU:HD13	1:B:454:TRP:CH2	0.68	2.22	10	20
1:A:451:LEU:HD23	1:B:418:HIS:CD2	0.68	2.22	17	3
1:B:433:LEU:HD12	1:B:452:LEU:HD21	0.68	1.65	20	10
1:A:406:LEU:CD1	1:B:433:LEU:HD23	0.68	2.18	21	3
1:A:452:LEU:HD22	1:B:422:LEU:HD12	0.68	1.64	6	13
1:A:422:LEU:HD12	1:B:452:LEU:HD22	0.68	1.65	11	12
1:A:433:LEU:HD12	1:A:452:LEU:HD21	0.67	1.65	20	10
1:A:418:HIS:HB2	1:A:421:LEU:HD11	0.67	1.65	14	12
1:A:413:ALA:HB1	1:A:418:HIS:HA	0.67	1.67	14	3
1:B:413:ALA:HB1	1:B:418:HIS:HA	0.67	1.66	14	3
1:B:405:LEU:C	1:B:405:LEU:HD13	0.66	2.16	28	3
1:B:418:HIS:HB2	1:B:421:LEU:HD11	0.66	1.65	14	12
1:A:419:GLN:O	1:A:421:LEU:HD12	0.66	1.89	6	2
1:A:433:LEU:HD23	1:B:406:LEU:CD2	0.66	2.21	28	1
1:A:414:LEU:HD13	1:A:415:ARG:N	0.65	2.06	27	1
1:A:452:LEU:HD22	1:B:422:LEU:CD2	0.65	2.21	19	1
1:B:419:GLN:O	1:B:421:LEU:HD12	0.65	1.91	6	2
1:A:451:LEU:HD21	1:B:414:LEU:HD21	0.65	1.69	20	2
1:A:406:LEU:CD2	1:B:433:LEU:HD23	0.65	2.21	28	1
1:B:414:LEU:HD13	1:B:415:ARG:N	0.65	2.06	27	1
1:A:418:HIS:NE2	1:B:451:LEU:HD23	0.65	2.07	17	3
1:A:451:LEU:O	1:B:421:LEU:HD12	0.65	1.91	16	8
1:B:405:LEU:HD13	1:B:405:LEU:C	0.65	2.17	2	25
1:A:405:LEU:C	1:A:405:LEU:HD13	0.65	2.16	28	3
1:A:405:LEU:HD13	1:A:405:LEU:C	0.65	2.17	15	25
1:A:422:LEU:CD2	1:B:452:LEU:HD22	0.65	2.21	19	1
1:B:441:THR:HG21	1:B:447:GLU:HB3	0.64	1.69	20	21
1:A:405:LEU:HD22	1:A:405:LEU:O	0.64	1.92	28	1
1:A:414:LEU:HD21	1:B:451:LEU:HD21	0.64	1.68	20	2
1:A:433:LEU:HD11	1:B:421:LEU:HD22	0.64	1.69	25	4
1:A:454:TRP:CE2	1:B:422:LEU:HD13	0.64	2.28	7	3
1:A:421:LEU:HD12	1:B:451:LEU:O	0.63	1.93	16	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:441:THR:HG21	1:A:447:GLU:HB3	0.63	1.69	20	20
1:A:421:LEU:HD22	1:B:433:LEU:HD11	0.63	1.70	21	4
1:B:405:LEU:O	1:B:405:LEU:HD22	0.63	1.92	28	1
1:A:451:LEU:HD23	1:B:418:HIS:NE2	0.63	2.09	17	3
1:A:414:LEU:HD22	1:A:414:LEU:C	0.62	2.20	27	1
1:B:448:ALA:O	1:B:452:LEU:HD12	0.62	1.94	16	14
1:B:414:LEU:HD13	1:B:414:LEU:C	0.62	2.20	27	1
1:A:414:LEU:HD13	1:A:414:LEU:C	0.62	2.19	27	1
1:A:448:ALA:O	1:A:452:LEU:HD12	0.61	1.94	16	15
1:B:414:LEU:HD22	1:B:414:LEU:C	0.60	2.20	27	1
1:A:422:LEU:HD21	1:B:433:LEU:CB	0.60	2.27	5	9
1:A:436:THR:HG21	1:B:410:ALA:HB3	0.60	1.74	23	7
1:A:433:LEU:CB	1:B:422:LEU:HD21	0.60	2.27	5	9
1:A:422:LEU:HD13	1:B:454:TRP:CE2	0.60	2.30	7	3
1:A:430:GLU:OE1	1:A:466:LEU:HD11	0.59	1.97	9	1
1:A:458:THR:HG22	1:A:462:LYS:HG3	0.59	1.75	7	2
1:A:451:LEU:HD22	1:B:414:LEU:HD11	0.59	1.73	25	3
1:B:430:GLU:HG2	1:B:466:LEU:HD11	0.59	1.75	6	2
1:A:430:GLU:HG2	1:A:466:LEU:HD11	0.58	1.75	6	1
1:B:458:THR:HG22	1:B:462:LYS:HG3	0.58	1.74	7	2
1:B:430:GLU:OE1	1:B:466:LEU:HD11	0.58	1.97	9	1
1:A:414:LEU:HD11	1:B:451:LEU:HD22	0.58	1.73	25	4
1:A:414:LEU:HD12	1:A:418:HIS:HB3	0.57	1.75	19	3
1:B:430:GLU:CD	1:B:466:LEU:HD11	0.57	2.25	18	1
1:B:414:LEU:HD12	1:B:418:HIS:HB3	0.57	1.75	19	3
1:B:406:LEU:HD12	1:B:409:TRP:CE3	0.57	2.34	28	1
1:A:430:GLU:CD	1:A:466:LEU:HD11	0.56	2.25	18	1
1:A:406:LEU:HD12	1:A:409:TRP:CE3	0.56	2.34	28	1
1:A:410:ALA:HB3	1:B:436:THR:HG21	0.56	1.74	23	7
1:A:452:LEU:HD22	1:B:422:LEU:HD23	0.56	1.77	19	1
1:A:433:LEU:HB3	1:B:422:LEU:HD21	0.56	1.78	2	8
1:A:452:LEU:HB3	1:B:422:LEU:HD12	0.56	1.78	7	3
1:A:422:LEU:HD21	1:B:433:LEU:HB3	0.55	1.78	17	8
1:A:402:TRP:HH2	1:A:425:ALA:HB1	0.54	1.62	28	1
1:A:422:LEU:HD23	1:B:452:LEU:HD22	0.54	1.78	19	1
1:B:427:PRO:CA	1:B:466:LEU:HD22	0.54	2.32	5	9
1:B:402:TRP:HH2	1:B:425:ALA:HB1	0.54	1.62	28	1
1:A:429:LEU:CD1	1:B:402:TRP:CZ3	0.54	2.91	2	3
1:A:451:LEU:HD13	1:B:418:HIS:CE1	0.54	2.38	8	1
1:A:427:PRO:CA	1:A:466:LEU:HD22	0.54	2.33	5	10
1:A:422:LEU:HD12	1:B:452:LEU:HB3	0.54	1.80	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:402:TRP:CZ3	1:B:429:LEU:CD1	0.53	2.91	2	2
1:A:418:HIS:CE1	1:B:451:LEU:HD13	0.53	2.38	8	1
1:B:413:ALA:HB1	1:B:418:HIS:CG	0.53	2.39	22	1
1:A:425:ALA:CB	1:B:429:LEU:HD11	0.53	2.31	18	2
1:A:402:TRP:HZ3	1:B:429:LEU:HD12	0.52	1.65	4	3
1:A:413:ALA:HB1	1:A:418:HIS:CG	0.52	2.39	22	1
1:A:418:HIS:CE1	1:B:451:LEU:HD23	0.52	2.40	4	1
1:B:463:LEU:C	1:B:463:LEU:HD23	0.52	2.30	15	5
1:A:433:LEU:HD23	1:B:406:LEU:HD11	0.52	1.82	24	3
1:A:454:TRP:CZ2	1:B:422:LEU:CD1	0.52	2.92	9	3
1:A:463:LEU:C	1:A:463:LEU:HD23	0.51	2.30	15	5
1:A:414:LEU:HD12	1:A:418:HIS:CB	0.51	2.35	4	2
1:B:414:LEU:HD12	1:B:418:HIS:CB	0.51	2.36	4	2
1:A:451:LEU:HD23	1:B:418:HIS:CE1	0.51	2.41	4	1
1:A:406:LEU:HD11	1:B:433:LEU:HD23	0.51	1.83	24	3
1:A:414:LEU:HD11	1:B:451:LEU:CD2	0.51	2.36	25	2
1:A:402:TRP:CH2	1:A:425:ALA:HB1	0.51	2.40	28	1
1:A:414:LEU:HD23	1:B:440:HIS:CG	0.51	2.41	22	1
1:A:429:LEU:HD11	1:B:425:ALA:CB	0.50	2.31	18	2
1:A:440:HIS:CG	1:B:414:LEU:HD23	0.50	2.41	22	1
1:A:451:LEU:CD2	1:B:414:LEU:HD11	0.50	2.37	25	1
1:A:440:HIS:CD2	1:B:414:LEU:HD21	0.50	2.41	27	2
1:B:402:TRP:CH2	1:B:425:ALA:HB1	0.50	2.41	28	1
1:A:458:THR:HG22	1:A:462:LYS:HD2	0.50	1.83	20	1
1:A:414:LEU:HD21	1:B:440:HIS:CD2	0.50	2.42	27	2
1:B:434:LEU:HD11	1:B:459:LEU:HD21	0.50	1.83	20	1
1:A:402:TRP:CH2	1:B:429:LEU:CD1	0.49	2.95	2	1
1:A:429:LEU:CD1	1:B:402:TRP:CH2	0.49	2.95	2	1
1:A:427:PRO:N	1:A:466:LEU:HD22	0.49	2.22	4	8
1:B:427:PRO:N	1:B:466:LEU:HD22	0.49	2.22	4	8
1:A:422:LEU:CD1	1:B:454:TRP:CZ2	0.49	2.92	9	5
1:A:410:ALA:CB	1:B:436:THR:HG21	0.49	2.37	18	2
1:A:436:THR:HG21	1:B:410:ALA:CB	0.49	2.37	18	2
1:A:418:HIS:CD2	1:A:418:HIS:O	0.49	2.66	14	4
1:B:458:THR:HG22	1:B:462:LYS:HD2	0.49	1.83	20	1
1:B:414:LEU:CD1	1:B:421:LEU:HD11	0.49	2.38	4	2
1:B:418:HIS:O	1:B:418:HIS:CD2	0.49	2.66	14	4
1:A:434:LEU:HD11	1:A:459:LEU:HD21	0.49	1.83	20	1
1:B:449:ALA:CA	1:B:459:LEU:CD1	0.49	2.91	5	26
1:A:449:ALA:CA	1:A:459:LEU:CD1	0.49	2.91	5	27
1:A:432:THR:HG22	1:B:406:LEU:HD12	0.48	1.85	20	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:429:LEU:HD12	1:B:402:TRP:HZ3	0.48	1.65	4	4
1:A:426:GLN:CB	1:A:427:PRO:CD	0.48	2.91	16	27
1:A:402:TRP:CB	1:B:402:TRP:CB	0.48	2.91	19	1
1:B:426:GLN:CB	1:B:427:PRO:CD	0.48	2.91	16	27
1:A:414:LEU:CD1	1:A:421:LEU:HD11	0.48	2.38	4	2
1:A:406:LEU:HD12	1:B:432:THR:HG22	0.48	1.85	20	4
1:B:452:LEU:O	1:B:454:TRP:CD1	0.47	2.67	4	7
1:A:409:TRP:CZ2	1:A:424:GLU:OE1	0.47	2.68	11	2
1:A:452:LEU:O	1:A:454:TRP:CD1	0.47	2.67	4	6
1:A:437:ALA:HB1	1:A:451:LEU:HD13	0.47	1.86	7	1
1:A:449:ALA:N	1:A:459:LEU:CD1	0.47	2.78	26	4
1:B:444:HIS:N	1:B:444:HIS:CD2	0.47	2.83	12	1
1:B:437:ALA:HB1	1:B:451:LEU:HD13	0.47	1.86	7	1
1:A:427:PRO:CB	1:A:466:LEU:HD22	0.47	2.40	13	1
1:B:409:TRP:CZ2	1:B:424:GLU:OE1	0.46	2.68	11	2
1:A:402:TRP:HB2	1:B:402:TRP:CD1	0.46	2.46	22	3
1:A:422:LEU:CD2	1:B:433:LEU:CB	0.46	2.93	26	1
1:B:449:ALA:N	1:B:459:LEU:CD1	0.46	2.78	26	4
1:B:427:PRO:CB	1:B:466:LEU:HD22	0.46	2.40	13	1
1:A:402:TRP:CD1	1:B:402:TRP:HB2	0.46	2.46	22	3
1:A:444:HIS:O	1:A:446:GLN:N	0.46	2.49	24	7
1:A:433:LEU:CD2	1:B:406:LEU:CD1	0.46	2.92	26	3
1:A:426:GLN:N	1:A:427:PRO:HD2	0.46	2.26	3	28
1:B:426:GLN:N	1:B:427:PRO:HD2	0.46	2.26	3	27
1:A:406:LEU:CD1	1:B:433:LEU:CD2	0.46	2.94	24	3
1:B:405:LEU:C	1:B:405:LEU:CD1	0.45	2.89	6	27
1:B:444:HIS:O	1:B:446:GLN:N	0.45	2.49	19	7
1:A:402:TRP:CD1	1:B:402:TRP:CB	0.45	3.00	22	2
1:A:414:LEU:HD23	1:B:440:HIS:CB	0.45	2.42	22	1
1:A:445:LYS:O	1:A:448:ALA:HB3	0.45	2.11	4	1
1:A:402:TRP:CB	1:B:402:TRP:CD1	0.45	2.99	22	2
1:A:405:LEU:C	1:A:405:LEU:CD1	0.45	2.90	4	26
1:A:413:ALA:HB1	1:A:418:HIS:ND1	0.45	2.27	22	1
1:A:444:HIS:N	1:A:444:HIS:CD2	0.45	2.83	12	1
1:B:413:ALA:HB1	1:B:418:HIS:ND1	0.45	2.27	22	1
1:B:405:LEU:O	1:B:409:TRP:CB	0.44	2.66	19	23
1:A:405:LEU:O	1:A:409:TRP:CB	0.44	2.66	5	23
1:B:445:LYS:O	1:B:448:ALA:HB3	0.44	2.12	4	1
1:B:422:LEU:CD2	1:B:422:LEU:N	0.44	2.81	19	1
1:A:418:HIS:O	1:A:418:HIS:ND1	0.43	2.51	17	1
1:B:429:LEU:HD23	1:B:430:GLU:OE1	0.43	2.13	21	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:433:LEU:CB	1:B:422:LEU:CD2	0.43	2.96	26	1
1:A:419:GLN:O	1:A:421:LEU:N	0.43	2.52	19	8
1:A:410:ALA:O	1:A:414:LEU:CB	0.43	2.67	27	1
1:A:451:LEU:HD22	1:B:414:LEU:HD21	0.43	1.90	5	1
1:A:409:TRP:CH2	1:A:421:LEU:HA	0.43	2.49	24	2
1:B:409:TRP:CH2	1:B:421:LEU:HA	0.43	2.48	21	2
1:B:402:TRP:CH2	1:B:406:LEU:HD22	0.43	2.49	28	1
1:A:418:HIS:C	1:A:418:HIS:CD2	0.43	2.97	20	1
1:A:452:LEU:HD22	1:B:422:LEU:HD21	0.43	1.89	19	1
1:A:422:LEU:CD2	1:A:422:LEU:N	0.43	2.81	19	1
1:A:441:THR:O	1:A:442:GLN:C	0.43	2.62	3	18
1:A:420:ASN:OD1	1:A:420:ASN:N	0.43	2.52	6	1
1:A:433:LEU:HD12	1:A:452:LEU:HD22	0.43	1.90	15	2
1:A:429:LEU:HD23	1:A:430:GLU:OE1	0.43	2.13	21	1
1:A:402:TRP:CH2	1:A:406:LEU:HD22	0.43	2.49	28	1
1:B:438:LEU:O	1:B:441:THR:N	0.43	2.52	13	22
1:B:420:ASN:N	1:B:420:ASN:OD1	0.43	2.52	6	1
1:B:418:HIS:O	1:B:418:HIS:ND1	0.43	2.51	17	1
1:B:410:ALA:O	1:B:414:LEU:CB	0.43	2.66	27	1
1:A:406:LEU:HD13	1:B:433:LEU:HD23	0.43	1.89	21	1
1:A:438:LEU:O	1:A:441:THR:N	0.42	2.52	20	25
1:B:433:LEU:HD12	1:B:452:LEU:HD22	0.42	1.90	15	2
1:B:441:THR:O	1:B:442:GLN:C	0.42	2.62	3	21
1:B:419:GLN:O	1:B:421:LEU:N	0.42	2.52	19	8
1:B:418:HIS:CD2	1:B:418:HIS:C	0.42	2.97	20	1
1:A:440:HIS:CB	1:B:414:LEU:HD23	0.42	2.42	22	1
1:A:420:ASN:N	1:A:420:ASN:OD1	0.42	2.52	8	1
1:A:440:HIS:ND1	1:A:451:LEU:HD11	0.42	2.30	15	1
1:A:433:LEU:HB2	1:B:422:LEU:HD21	0.42	1.92	20	1
1:A:438:LEU:O	1:A:442:GLN:N	0.42	2.53	24	7
1:A:418:HIS:O	1:A:418:HIS:CG	0.42	2.73	14	1
1:B:418:HIS:O	1:B:418:HIS:CG	0.42	2.73	14	1
1:A:418:HIS:CE1	1:B:451:LEU:HA	0.42	2.49	17	1
1:A:402:TRP:CB	1:B:402:TRP:HB2	0.42	2.45	19	1
1:A:434:LEU:O	1:A:438:LEU:CB	0.42	2.67	20	3
1:B:438:LEU:O	1:B:442:GLN:N	0.42	2.53	9	6
1:B:443:GLY:O	1:B:445:LYS:N	0.42	2.53	21	1
1:B:402:TRP:O	1:B:405:LEU:N	0.42	2.52	23	1
1:B:449:ALA:HB1	1:B:455:GLY:CA	0.42	2.44	3	1
1:B:414:LEU:C	1:B:414:LEU:CD1	0.42	2.90	27	1
1:B:461:ALA:O	1:B:465:GLU:CG	0.42	2.68	28	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:422:LEU:CD1	1:B:454:TRP:CH2	0.42	3.02	1	1
1:A:414:LEU:HD21	1:B:451:LEU:HD22	0.42	1.91	5	1
1:B:420:ASN:OD1	1:B:420:ASN:N	0.42	2.52	8	1
1:A:451:LEU:CD2	1:B:414:LEU:HD21	0.42	2.45	14	1
1:A:402:TRP:HB2	1:B:402:TRP:CB	0.42	2.45	19	1
1:A:457:ALA:O	1:A:461:ALA:CB	0.42	2.68	20	2
1:A:438:LEU:HD13	1:A:445:LYS:HA	0.42	1.92	15	2
1:A:447:GLU:N	1:A:447:GLU:OE1	0.41	2.53	8	1
1:B:447:GLU:CA	1:B:447:GLU:OE1	0.41	2.68	13	1
1:B:444:HIS:CD2	1:B:447:GLU:HG3	0.41	2.50	24	1
1:B:434:LEU:O	1:B:438:LEU:CB	0.41	2.69	5	4
1:A:451:LEU:HA	1:B:418:HIS:CE1	0.41	2.50	17	1
1:A:451:LEU:O	1:B:421:LEU:CD1	0.41	2.68	21	1
1:B:427:PRO:HA	1:B:466:LEU:HD13	0.41	1.91	16	2
1:A:430:GLU:O	1:A:434:LEU:CB	0.41	2.69	21	1
1:B:444:HIS:ND1	1:B:447:GLU:OE2	0.41	2.54	27	1
1:B:457:ALA:O	1:B:461:ALA:CB	0.41	2.68	20	2
1:A:402:TRP:O	1:A:405:LEU:N	0.41	2.53	23	1
1:A:449:ALA:HB1	1:A:455:GLY:CA	0.41	2.45	3	1
1:A:433:LEU:HD23	1:B:406:LEU:HD13	0.41	1.89	21	1
1:A:441:THR:HG22	1:A:447:GLU:OE2	0.41	2.15	22	1
1:A:443:GLY:O	1:A:445:LYS:N	0.41	2.53	21	1
1:B:430:GLU:O	1:B:434:LEU:CB	0.41	2.69	21	1
1:B:423:SER:O	1:B:427:PRO:CD	0.41	2.69	22	1
1:A:402:TRP:O	1:A:403:ALA:C	0.41	2.63	23	1
1:A:461:ALA:O	1:A:465:GLU:CG	0.41	2.68	28	1
1:B:413:ALA:O	1:B:418:HIS:N	0.41	2.54	14	2
1:A:427:PRO:HA	1:A:466:LEU:HD13	0.41	1.91	16	1
1:A:444:HIS:ND1	1:A:447:GLU:OE2	0.41	2.53	27	1
1:B:440:HIS:ND1	1:B:451:LEU:HD11	0.41	2.30	15	1
1:A:414:LEU:C	1:A:414:LEU:CD1	0.41	2.90	27	1
1:A:413:ALA:O	1:A:418:HIS:N	0.41	2.54	6	1
1:B:447:GLU:OE1	1:B:447:GLU:N	0.41	2.54	8	1
1:A:444:HIS:O	1:A:445:LYS:CB	0.41	2.69	9	2
1:A:414:LEU:HD21	1:B:451:LEU:CD2	0.41	2.45	14	1
1:B:438:LEU:HD13	1:B:445:LYS:HA	0.41	1.92	17	1
1:A:444:HIS:CD2	1:A:447:GLU:HG3	0.41	2.50	24	1
1:A:421:LEU:CD1	1:B:451:LEU:O	0.40	2.68	3	2
1:A:433:LEU:HD11	1:B:421:LEU:HB3	0.40	1.93	6	1
1:B:427:PRO:CD	1:B:466:LEU:HD22	0.40	2.47	13	1
1:B:422:LEU:O	1:B:426:GLN:CG	0.40	2.69	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:420:ASN:ND2	1:A:423:SER:CB	0.40	2.84	20	1
1:B:420:ASN:ND2	1:B:423:SER:CB	0.40	2.84	20	1
1:B:441:THR:HG22	1:B:447:GLU:OE2	0.40	2.16	22	1
1:A:458:THR:O	1:A:462:LYS:CB	0.40	2.69	16	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	66/91 (73%)	56±1 (85±2%)	8±1 (12±2%)	2±1 (2±2%)	7	44
1	B	66/91 (73%)	56±1 (85±2%)	8±2 (12±2%)	2±1 (2±2%)	7	44
All	All	3696/5096 (73%)	3147 (85%)	461 (12%)	88 (2%)	7	44

All 16 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	417	GLY	15
1	B	417	GLY	15
1	A	420	ASN	9
1	B	420	ASN	9
1	A	416	SER	6
1	A	419	GLN	6
1	B	416	SER	6
1	B	419	GLN	6
1	A	421	LEU	4
1	B	421	LEU	4
1	A	418	HIS	2
1	B	418	HIS	2
1	A	449	ALA	1
1	B	449	ALA	1
1	A	445	LYS	1
1	B	445	LYS	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	50/73 (68%)	34±3 (68±5%)	16±3 (32±5%)	1	14
1	B	50/73 (68%)	34±3 (68±5%)	16±3 (32±5%)	1	14
All	All	2800/4088 (68%)	1908 (68%)	892 (32%)	1	14

All 70 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	433	LEU	28
1	A	459	LEU	28
1	B	433	LEU	28
1	B	459	LEU	28
1	A	402	TRP	27
1	A	414	LEU	27
1	B	402	TRP	27
1	B	414	LEU	27
1	A	430	GLU	24
1	B	430	GLU	24
1	A	421	LEU	20
1	B	421	LEU	20
1	A	451	LEU	19
1	B	451	LEU	19
1	A	429	LEU	17
1	B	429	LEU	17
1	A	464	LYS	16
1	B	464	LYS	16
1	A	447	GLU	16
1	B	447	GLU	16
1	A	419	GLN	15
1	B	419	GLN	15
1	A	445	LYS	14
1	B	445	LYS	14
1	A	442	GLN	14
1	B	442	GLN	14
1	A	412	ARG	12
1	A	423	SER	12

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Mol	Chain	Res	Type	Models (Total)
1	B	412	ARG	12
1	B	423	SER	12
1	A	431	ARG	11
1	B	431	ARG	11
1	A	416	SER	11
1	B	416	SER	11
1	A	428	GLU	11
1	B	428	GLU	11
1	A	424	GLU	10
1	B	424	GLU	10
1	A	439	ARG	10
1	B	439	ARG	10
1	A	446	GLN	10
1	B	446	GLN	10
1	A	450	ARG	9
1	B	450	ARG	9
1	A	465	GLU	9
1	B	465	GLU	9
1	A	463	LEU	9
1	B	463	LEU	9
1	A	408	GLN	9
1	B	408	GLN	9
1	A	444	HIS	8
1	A	462	LYS	8
1	B	444	HIS	8
1	B	462	LYS	8
1	A	426	GLN	8
1	B	426	GLN	8
1	A	434	LEU	8
1	B	434	LEU	8
1	A	415	ARG	7
1	B	415	ARG	7
1	A	411	ASP	6
1	B	411	ASP	6
1	A	406	LEU	5
1	B	406	LEU	5
1	A	418	HIS	4
1	B	418	HIS	4
1	A	404	THR	3
1	B	404	THR	3
1	A	405	LEU	1
1	B	405	LEU	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided